Qiong Yang

List of Publications by Year
in descending order

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124 papers	18,553 citations	26630 56 h-index	17105 122 g-index
133 all docs	133 docs citations	133 times ranked	25578 citing authors

#	Article	IF	Citations
1	Genetic meta-analysis of diagnosed Alzheimerâ€™s disease identifies new risk loci and implicates AÎ², tau, immunity and lipid processing. Nature Genetics, 2019, 51, 414-430.	21.4	1,962
2	Common variants at 30 loci contribute to polygenic dyslipidemia. Nature Genetics, 2009, 41, 56-65.	21.4	1,234
3	Multiancestry genome-wide association study of 520,000 subjects identifies 32 loci associated with stroke and stroke subtypes. Nature Genetics, 2018, 50, 524-537.	21.4	1,124
4	Rare coding variants in PLCG2, ABI3, and TREM2 implicate microglial-mediated innate immunity in Alzheimer's disease. Nature Genetics, 2017, 49, 1373-1384.	21.4	783
5	The Third Generation Cohort of the National Heart, Lung, and Blood Institute's Framingham Heart Study: Design, Recruitment, and Initial Examination. American Journal of Epidemiology, 2007, 165, 1328-1335.	3.4	752
6	New loci associated with kidney function and chronic kidney disease. Nature Genetics, 2010, 42, 376-384.	21.4	710
7	New insights into the genetic etiology of Alzheimerâ€™s disease and related dementias. Nature Genetics, 2022, 54, 412-436.	21.4	700
8	Genome-wide association analyses identify 18 new loci associated with serum urate concentrations. Nature Genetics, 2013, 45, 145-154.	21.4	675
9	Association of three genetic loci with uric acid concentration and risk of gout: a genome-wide association study. Lancet, The, 2008, 372, 1953-1961.	13.7	610
10	Multiple loci associated with indices of renal function and chronic kidney disease. Nature Genetics, 2009, 41, 712-717.	21.4	553
11	A catalog of genetic loci associated with kidney function from analyses of a million individuals. Nature Genetics, 2019, 51, 957-972.	21.4	549
12	Study of 300,486 individuals identifies 148 independent genetic loci influencing general cognitive function. Nature Communications, 2018, 9, 2098.	12.8	484
13	The genetic architecture of the human cerebral cortex. Science, 2020, 367, .	12.6	450
14	Genetic associations at 53 loci highlight cell types and biological pathways relevant for kidney function. Nature Communications, 2016, 7, 10023.	12.8	412
15	Multiple loci influence erythrocyte phenotypes in the CHARGE Consortium. Nature Genetics, 2009, 41, 1191-1198.	21.4	324
16	Multiple Genetic Loci Influence Serum Urate Levels and Their Relationship With Gout and Cardiovascular Disease Risk Factors. Circulation: Cardiovascular Genetics, 2010, 3, 523-530.	5.1	285
17	Large-scale analyses of common and rare variants identify 12 new loci associated with atrial fibrillation. Nature Genetics, 2017, 49, 946-952.	21.4	279
18	Target genes, variants, tissues and transcriptional pathways influencing human serum urate levels. Nature Genetics, 2019, 51, 1459-1474.	21.4	251

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19	Genome-wide meta-analyses identifies seven loci associated with platelet aggregation in response to agonists. Nature Genetics, 2010, 42, 608-613.	21.4	247
20	A Combined Epidemiologic and Metabolomic Approach Improves CKD Prediction. Journal of the American Society of Nephrology: JASN, 2013, 24, 1330-1338.	6.1	233
21	GWAF: an R package for genome-wide association analyses with family data. Bioinformatics, 2010, 26, 580-581.	4.1	220
22	CUBN Is a Gene Locus for Albuminuria. Journal of the American Society of Nephrology: JASN, 2011, 22, 555-570.	6.1	208
23	Genetic architecture of subcortical brain structures in 38,851 individuals. Nature Genetics, 2019, 51, 1624-1636.	21.4	192
24	Genome-Wide Association Studies of Serum Magnesium, Potassium, and Sodium Concentrations Identify Six Loci Influencing Serum Magnesium Levels. PLoS Genetics, 2010, 6, e1001045.	3.5	185
25	Association of eGFR-Related Loci Identified by GWAS with Incident CKD and ESRD. PLoS Genetics, 2011, 7, e1002292.	3.5	172
26	The Framingham Heart Study 100K SNP genome-wide association study resource: overview of 17 phenotype working group reports. BMC Medical Genetics, 2007, 8, S1.	2.1	169
27	Genome-Wide Association and Functional Follow-Up Reveals New Loci for Kidney Function. PLoS Genetics, 2012, 8, e1002584.	3.5	166
28	Multiethnic Genome-Wide Association Study of Cerebral White Matter Hyperintensities on MRI. Circulation: Cardiovascular Genetics, 2015, 8, 398-409.	5.1	162
29	Genomewide Linkage Analysis to Serum Creatinine, GFR, and Creatinine Clearance in a Community-Based Population. Journal of the American Society of Nephrology: JASN, 2004, 15, 2457-2461.	6.1	161
30	Epigenome-wide association studies identify DNA methylation associated with kidney function. Nature Communications, 2017, 8, 1286.	12.8	145
31	Circulating metabolites and general cognitive ability and dementia: Evidence from 11 cohort studies. Alzheimer's and Dementia, 2018, 14, 707-722.	0.8	143
32	Common variants in Alzheimerâ€™s disease and risk stratification by polygenic risk scores. Nature Communications, 2021, 12, 3417.	12.8	140
33	Candidate Gene Association Resource (CARe). Circulation: Cardiovascular Genetics, 2010, 3, 267-275.	5.1	139
34	Causal Assessment of Serum Urate Levels inÂCardiometabolic Diseases Through a Mendelian Randomization Study. Journal of the American College of Cardiology, 2016, 67, 407-416.	2.8	138
35	Analyze multivariate phenotypes in genetic association studies by combining univariate association tests. Genetic Epidemiology, 2010, 34, 444-454.	1.3	137
36	Genome-wide association meta-analyses and fine-mapping elucidate pathways influencing albuminuria. Nature Communications, 2019, 10, 4130.	12.8	133

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37	Genome-wide Association Studies Identify Genetic Loci Associated With Albuminuria in Diabetes. Diabetes, 2016, 65, 803-817.	0.6	131
38	Dimethylguanidino valeric acid is a marker of liver fat and predicts diabetes. Journal of Clinical Investigation, 2017, 127, 4394-4402.	8.2	115
39	Genome-wide search for genes affecting serum uric acid levels: the Framingham Heart Study. Metabolism: Clinical and Experimental, 2005, 54, 1435-1441.	3.4	101
40	Genome-wide association study for serum urate concentrations and gout among African Americans identifies genomic risk loci and a novel URAT1 loss-of-function allele. Human Molecular Genetics, 2011, 20, 4056-4068.	2.9	101
41	1000 Genomes-based meta-analysis identifies 10 novel loci for kidney function. Scientific Reports, 2017, 7, 45040.	3.3	98
42	Methods for Analyzing Multivariate Phenotypes in Genetic Association Studies. Journal of Probability and Statistics, 2012, 2012, 1-13.	0.7	90
43	Genome-wide association study for circulating levels of PAI-1 provides novel insights into its regulation. Blood, 2012, 120, 4873-4881.	1.4	90
44	Association of Novel Genetic Loci With Circulating Fibrinogen Levels. Circulation: Cardiovascular Genetics, 2009, 2, 125-133.	5.1	86
45	Association of Alzheimer's disease GWAS loci with MRI markers of brain aging. Neurobiology of Aging, 2015, 36, 1765.e7-1765.e16.	3.1	82
46	A genome-wide association for kidney function and endocrine-related traits in the NHLBI's Framingham Heart Study. BMC Medical Genetics, 2007, 8, S10.	2.1	80
47	Identification of cis - and trans -Acting Genetic Variants Explaining Up to Half the Variation in Circulating Vascular Endothelial Growth Factor Levels. Circulation Research, 2011, 109, 554-563.	4.5	72
48	Common Genetic Variation Indicates Separate Causes for Periventricular and Deep White Matter Hyperintensities. Stroke, 2020, 51, 2111-2121.	2.0	71
49	Comprehensive Survey of Common Genetic Variation at the Plasminogen Activator Inhibitor-1 Locus and Relations to Circulating Plasminogen Activator Inhibitor-1 Levels. Circulation, 2005, 112, 1728-1735.	1.6	70
50	Genome-Wide Meta-Analysis of Homocysteine and Methionine Metabolism Identifies Five One Carbon Metabolism Loci and a Novel Association of ALDH1L1 with Ischemic Stroke. PLoS Genetics, 2014, 10, e1004214.	3.5	69
51	An exome array study of the plasma metabolome. Nature Communications, 2016, 7, 12360.	12.8	69
52	Genome-wide association and linkage analyses of hemostatic factors and hematological phenotypes in the Framingham Heart Study. BMC Medical Genetics, 2007, 8, S12.	2.1	66
53	Integration of genome-wide association studies with biological knowledge identifies six novel genes related to kidney function. Human Molecular Genetics, 2012, 21, 5329-5343.	2.9	64
54	Genetic Architecture of the Cardiovascular Risk Proteome. Circulation, 2018, 137, 1158-1172.	1.6	64

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55	Lipid and lipoprotein measurements and the risk of ischemic vascular events. Neurology, 2015, 84, 472-479.	1.1	62
56	Association of Single Nucleotide Polymorphisms on Chromosome 9p21.3 With Platelet Reactivity. Circulation: Cardiovascular Genetics, 2010, 3, 445-453.	5.1	61
57	Genetic correlations and genome-wide associations of cortical structure in general population samples of 22,824 adults. Nature Communications, 2020, 11, 4796.	12.8	61
58	Genetic Predictors of Fibrin D-Dimer Levels in Healthy Adults. Circulation, 2011, 123, 1864-1872.	1.6	60
59	Common Genetic Variation in Five Thrombosis Genes and Relations to Plasma Hemostatic Protein Level and Cardiovascular Disease Risk. Arteriosclerosis, Thrombosis, and Vascular Biology, 2006, 26, 1405-1412.	2.4	59
60	Clinical and Genetic Correlates of Circulating Angiopoietin-2 and Soluble Tie-2 in the Community. Circulation: Cardiovascular Genetics, 2010, 3, 300-306.	5.1	55
61	Profiling of the plasma proteome across different stages of human heart failure. Nature Communications, 2019, 10, 5830.	12.8	53
62	CDKN1C/p57kip2is a candidate tumor suppressor gene in human breast cancer. BMC Cancer, 2008, 8, 68.	2.6	50
63	Maternal influence on blood pressure suggests involvement of mitochondrial DNA in the pathogenesis of hypertension: the Framingham Heart Study. Journal of Hypertension, 2007, 25, 2067-2073.	0.5	47
64	Quantitative DNA Fingerprinting May Distinguish New Primary Breast Cancer From Disease Recurrence. Journal of Clinical Oncology, 2004, 22, 1830-1838.	1.6	45
65	Genome-wide linkage analysis to urinary microalbuminuria in a community-based sample: The Framingham Heart Study. Kidney International, 2005, 67, 70-74.	5.2	44
66	Assessment of Genetic Determinants of the Association of Î³â€² Fibrinogen in Relation to Cardiovascular Disease. Arteriosclerosis, Thrombosis, and Vascular Biology, 2011, 31, 2345-2352.	2.4	44
67	Large-scale whole-exome sequencing association studies identify rare functional variants influencing serum urate levels. Nature Communications, 2018, 9, 4228.	12.8	43
68	Probing the Virtual Proteome to Identify Novel Disease Biomarkers. Circulation, 2018, 138, 2469-2481.	1.6	42
69	Proteomics Profiling and Risk of Newâ€Onset Atrial Fibrillation: Framingham Heart Study. Journal of the American Heart Association, 2019, 8, e010976.	3.7	42
70	Meta-analysis uncovers genome-wide significant variants for rapid kidney function decline. Kidney International, 2021, 99, 926-939.	5.2	42
71	Association of common genetic variants with brain microbleeds. Neurology, 2020, 95, e3331-e3343.	1.1	40
72	SOS2 and ACP1 Loci Identified through Large-Scale Exome Chip Analysis Regulate Kidney Development and Function. Journal of the American Society of Nephrology: JASN, 2017, 28, 981-994.	6.1	39

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73	Association of Genetic Variation in the Mitochondrial Genome With Blood Pressure and Metabolic Traits. Hypertension, 2012, 60, 949-956.	2.7	38
74	Evidence for linkage of red blood cell size and count: Genome-wide scans in the Framingham Heart Study. American Journal of Hematology, 2007, 82, 605-610.	4.1	37
75	Association of variants inHTRA1andNOTCH3with MRI-defined extremes of cerebral small vessel disease in older subjects. Brain, 2019, 142, 1009-1023.	7.6	37
76	Association of genomic loci from a cardiovascular gene SNP array with fibrinogen levels in European Americans and African-Americans from six cohort studies: the Candidate Gene Association Resource (CARe). Blood, 2011, 117, 268-275.	1.4	36
77	Common Variants in Mendelian Kidney Disease Genes and Their Association with Renal Function. Journal of the American Society of Nephrology: JASN, 2013, 24, 2105-2117.	6.1	33
78	Genome-wide association study of 23,500 individuals identifies 7 loci associated with brain ventricular volume. Nature Communications, 2018, 9, 3945.	12.8	31
79	Genetic risk score and risk of stage 3 chronic kidney disease. BMC Nephrology, 2017, 18, 32.	1.8	30
80	A genome-wide search for genes affecting circulating fibrinogen levels in the Framingham Heart Study. Thrombosis Research, 2003, 110, 57-64.	1.7	29
81	A genome-wide association study identifies genetic loci associated with specific lobar brain volumes. Communications Biology, 2019, 2, 285.	4.4	27
82	Aptamer-Based Proteomic Platform Identifies Novel Protein Predictors of Incident Heart Failure and Echocardiographic Traits. Circulation: Heart Failure, 2020, 13, e006749.	3.9	26
83	Proteomic profiling reveals biomarkers and pathways in type 2 diabetes risk. JCI Insight, 2021, 6, .	5.0	26
84	Genome-wide association study reveals novel genetic loci: a new polygenic risk score for mitral valve prolapse. European Heart Journal, 2022, 43, 1668-1680.	2.2	25
85	Association of Circulating Metabolites in Plasma or Serum and Risk of Stroke. Neurology, 2021, 96, .	1.1	24
86	Association of Estimated Glomerular Filtration Rate and Urinary Uromodulin Concentrations with Rare Variants Identified by UMOD Gene Region Sequencing. PLoS ONE, 2012, 7, e38311.	2.5	24
87	Genome-wide linkage analyses and candidate gene fine mapping for HDL3 cholesterol: the Framingham Study. Journal of Lipid Research, 2005, 46, 1416-1425.	4.2	23
88	Description of the Framingham Heart Study data for Genetic Analysis Workshop 13. BMC Genetics, 2003, 4, S2.	2.7	22
89	Geneâ€centric approach identifies new and known loci for <scp>F</scp>VIII activity and <scp>VWF</scp> antigen levels in <scp>E</scp>uropean <scp>A</scp>mericans and <scp>A</scp>frican <scp>A</scp>mericans. American Journal of Hematology, 2015, 90, 534-540.	4.1	20
90	Plasma amyloid Î² levels are driven by genetic variants near APOE, BACE1, APP, PSEN2: A genomeâ€wide association study in over 12,000 nonâ€demented participants. Alzheimer's and Dementia, 2021, 17, 1663-1674.	0.8	20

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91	Circulating testican-2 is a podocyte-derived marker of kidney health. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 25026-25035.	7.1	19
92	Whole exome sequence-based association analyses of plasma amyloid-Î² in African and European Americans; the Atherosclerosis Risk in Communities-Neurocognitive Study. PLoS ONE, 2017, 12, e0180046.	2.5	18
93	Genetic loci and prioritization of genes for kidney function decline derived from a meta-analysis of 62 longitudinal genome-wide association studies. Kidney International, 2022, 102, 624-639.	5.2	18
94	Using Family-Based Imputation in Genome-Wide Association Studies with Large Complex Pedigrees: The Framingham Heart Study. PLoS ONE, 2012, 7, e51589.	2.5	17
95	Exome Chip Analysis Identifies Low-Frequency and Rare Variants in MRPL38 for White Matter Hyperintensities on Brain Magnetic Resonance Imaging. Stroke, 2018, 49, 1812-1819.	2.0	17
96	Circulating Metabolome and White Matter Hyperintensities in Women and Men. Circulation, 2022, 145, 1040-1052.	1.6	17
97	Differential and shared genetic effects on kidney function between diabetic and non-diabetic individuals. Communications Biology, 2022, 5, .	4.4	17
98	Flexible Semiparametric Analysis of Longitudinal Genetic Studies by Reduced Rank Smoothing. Journal of the Royal Statistical Society Series C: Applied Statistics, 2012, 61, 1-24.	1.0	16
99	Heritability of Mitral Regurgitation. Circulation: Cardiovascular Genetics, 2017, 10, .	5.1	16
100	A comparison of strategies for analyzing dichotomous outcomes in genome-wide association studies with general pedigrees. Genetic Epidemiology, 2011, 35, 650-657.	1.3	15
101	Multiomics integrative analysis identifies APOE allele-specific blood biomarkers associated to Alzheimerâ€™s disease etiopathogenesis. Aging, 2021, 13, 9277-9329.	3.1	15
102	The genetics of circulating BDNF: towards understanding the role of BDNF in brain structure and function in middle and old ages. Brain Communications, 2020, 2, fcaa176.	3.3	14
103	Proteomic Signatures of Lifestyle Risk Factors for Cardiovascular Disease: A Crossâ€Sectional Analysis of the Plasma Proteome in the Framingham Heart Study. Journal of the American Heart Association, 2021, 10, e018020.	3.7	14
104	Multiâ€phenotype analyses of hemostatic traits with cardiovascular events reveal novel genetic associations. Journal of Thrombosis and Haemostasis, 2022, 20, 1331-1349.	3.8	12
105	RVFam: an R package for rare variant association analysis with family data. Bioinformatics, 2016, 32, 624-626.	4.1	10
106	Genetic Architecture of Circulating Very-Long-Chain (C24:0 and C22:0) Ceramide Concentrations. Journal of Lipid and Atherosclerosis, 2020, 9, 172.	3.5	10
107	Genetic analyses of longitudinal phenotype data: a comparison of univariate methods and a multivariate approach. BMC Genetics, 2003, 4, S29.	2.7	9
108	A three-stage approach for genome-wide association studies with family data for quantitative traits. BMC Genetics, 2010, 11, 40.	2.7	8

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109	A genetic association study of D-dimer levels with 50K SNPs from a candidate gene chip in four ethnic groups. Thrombosis Research, 2014, 134, 462-467.	1.7	8
110	Blood Phosphorylated Tau 181 as a Biomarker for Amyloid Burden on Brain PET in Cognitively Healthy Adults. Journal of Alzheimer's Disease, 2022, 87, 1517-1526.	2.6	8
111	Handling linkage disequilibrium in linkage analysis using dense single-nucleotide polymorphisms. BMC Proceedings, 2007, 1, S161.	1.6	7
112	Multiomic Profiling in Black and White Populations Reveals Novel Candidate Pathways in Left Ventricular Hypertrophy and Incident Heart Failure Specific to Black Adults. Circulation Genomic and Precision Medicine, 2021, 14, e003191.	3.6	7
113	Allele-specific DNA methylation maps in monozygotic twins discordant for psychiatric disorders reveal that disease-associated switching at the EIPR1 regulatory loci modulates neural function. Molecular Psychiatry, 2021, 26, 6630-6642.	7.9	7
114	Gene-mapping study of extremes of cerebral small vessel disease reveals TRIM47 as a strong candidate. Brain, 2022, 145, 1992-2007.	7.6	6
115	Exome Array Analysis of Early-Onset Ischemic Stroke. Stroke, 2020, 51, 3356-3360.	2.0	5
116	An evaluation of approaches for rare variant association analyses of binary traits in related samples. Scientific Reports, 2021, 11, 3145.	3.3	5
117	Elucidating mechanisms of genetic cross-disease associations at the PROCR vascular disease locus. Nature Communications, 2022, 13, 1222.	12.8	5
118	Joint modeling of linkage and association using affected sib-pair data. BMC Proceedings, 2007, 1, S38.	1.6	3
119	Using linkage and association to identify and model genetic effects: summary of GAW15 Group 4. Genetic Epidemiology, 2007, 31, S34-S42.	1.3	3
120	Accelerometer-Measured, Habitual Physical Activity and Circulating Brain-Derived Neurotrophic Factor: A Cross-Sectional Study. Journal of Alzheimer's Disease, 2022, 85, 805-814.	2.6	2
121	Association of low-frequency and rare coding variants with information processing speed. Translational Psychiatry, 2021, 11, 613.	4.8	2
122	Effect of linkage disequilibrium between markers in linkage and association analyses. Genetic Epidemiology, 2007, 31, S139-S148.	1.3	1
123	Associations Between Brainstem Volume and Alzheimerâ€™s Disease Pathology in Middle-Aged Individuals of the Framingham Heart Study. Journal of Alzheimer's Disease, 2022, 86, 1603-1609.	2.6	0
124	Rare and Common Variants in COL4A1 in Chinese Patients With Intracerebral Hemorrhage. Frontiers in Neurology, 0, 13, .	2.4	0